Fig. 1

5`-ATGAGGTCAGAAGCCTTGCTGCTATATTTCACACTGCTACACTTTGCTGG 50
GGCTGGTTTCCCAGAAGATTCTGAGCCAATCAGTATTTCGCATGGCAACT 100
ATACAAAACAGTATCCGGTGTTTGTGGCCACAAGCCAGGACGGAACACC 150
ACACAGAGGCACAGGCTGGACATCCAGATGATTATGATCATGAACGGAAC 200
CCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGATATAGACACAT 250
CACACACGGAAGAAATTTATTGTAGCAAAAAACTGACATGGAAATCTAGA 300
CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTG 350
CCACAACTTTATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTG 400
TCTGTGGAACTAATGCCTTCAACCCTTCCTGCAGAAACTATAAGATGGAT 450
ACATTGGAACCATTCGGGGATGAATTCAGCGGAATGGCCAGATGCCCATA 500
TGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGAAAACTATACT 550
CAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT 600
CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAATGGTT 650
GAAAGAACCATACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACT 700
TCTTCTTCAGGGAAATAGCAGTGGAGTATAACACCATGGGAAAGGTAGTT 750
TTCCCAAGAGTGGCTCAGGTTTGTAAGAATGATATGGGAGGATCTCAAAG 800
AGTCCTGGAGAAACAGTGGACGTCGTTCCTGAAGGCGCGCTTGAACTGCT 850
CAGTTCCTGGAGACTCTCATTTTTATTTCAACATTCTCCAGGCAGTTACA 900
GATGTGATTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTTCTAC 950
ACCTTATAACAGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTG 1000
ACATTGCCAGTGTTTTTACTGGGAGATTCAAGGAACAGAAGTCTCCTGAT 1050
TCCACCTGGACACCAGTTCCTGATGAACGAGTTCCTAAGCCCAGGCCAGG 1100
TTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAACCTCCAATGAGT 1150
TCCCTGATGATACCCTGAACTTCATCAAGACGCACCCGCTCATGGATGAG 1200
GCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAG 1250
ATACCGCCTTACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGA 1300
ATCACACTGTGGTTTTTCTGGGATCAGAGAAGGGAATCATCTTGAAGTTT 1350
TTGGCCAGAATAGGAAATAGTGGTTTTCTAAATGACAGCCTTTTCCTGGA 1400
GGAGATGAGTGTTTACAACTCTGAAAAATGCAGCTATGATGGAGTCGAAG 1450
ACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT 1500
GTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCCTTGGCCGGTGTGAACG 1550
ACATGGGAAGTGTAAAAAAACCTGTATTGCCTCCAGAGACCCATATTGTG 1600
GATGGATAAAGGAAGGTGGTGCCTGCAGCCATTTATCACCCAACAGCAGA 1650

Fig. 1 (cont.)

CTGACTTTTGAGCAGGACATAGAGCGTGGCAATACAGATGGTCTGGGGGA	1700
CTGTCACAATTCCTTTGTGGCACTGAATGGGCATTCCAGTTCCCTCTTGC	1750
CCAGCACAACCACATCAGATTCGACGGCTCAAGAGGGGTATGAGTCTAGG	1800
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TTGGCCATTGCAGTCATCCTGGCTTTCGTCATGGGGGCCGTCTTCTCGGG	2000
CATCACCGTCTACTGCGTCTGTGATCATCGGCGCAAAGACGTGGCTGTGG	2050
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AAAGCCGGAGGCCATCCTCACGCCACTCATGCACAACGGCAAGCTCGCCA	2200
CTCCCGGCAACACGGCCAAGATGCTCATTAAAGCAGACCAGCACCACCTG	2250
GACCTGACGGCCCTCCCCACCCCAGAGTCAACCCCAACGCTGCAGCAGAA	2300
GCGGAAGCCCAGCCGCGGCAGCCGCGAGTGGGAGAGGAACCAGAACCTCA	2350
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CCTGCCCATCACGCAGCAGGGCTACCAGCATGAGTACGTGGACCAGCCCA	2500
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GAGTATAAGACCATCAAGGAACATCTCAGCAGCAAGAGTCCCAACCATGG	2600
GGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCCCAAAGTTCCACAGC	2650
GGGAGGCCTCCCTGGGTCCCCCGGGAGCCTCCCTGTCTCAGACCGGTCTA	2700
AGCAAGCGGCTGGAAATGCACCACTCCTCTTCCTACGGGGTTGACTATAA	2750
GAGGAGCTACCCCACGAACTCGCTCACGAGAAGCCACCAGGCCACCACTC	2800
TCAAAAGAAACAACACTAACTCCTCCAATTCCTCTCACCTCTCCAGAAAC	2850
CAGAGCTTTGGCAGGGGAGACAACCCGCCGCCCGCCCCGCAGAGGGTGGA	2900
CTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGGCCGTGACTGTCT	2950
CGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCGGGGCTG	3000
AAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGC	3050
TCCCCTTTCCACATCCATGAAGCCCAATGATGCGTGTACATAA-3`	3093

09/856681

Fig. 2

```
   ggcacgaggctgcagccaactccgctccccgcgcactcggctgcccaggcgctcgga   57
acccagcagcggcgctcctccgcggtgccggtcgcccgcgatgcccgcttagcagcgtgt  117
agcagcggccagcatcaccacacccgcggcaccgcgctgccggccgcagagccgggccag  177
agccttgccccctcccccagcccccaccccgcccccgccctgaaatgacttgttaatc  237
ggcgcagacaccaccaaggggactcaccgaagtggaatccaagtggaatttggatttgga  297
gaagagtttcttgaacatttaccctcttccttgttggttttctttttctttttcttcttt  357
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cgataatggattactaaatgggatacacgctgtaccagttcgctccgagccccggccgcc  597
tgtccgtcgatgcaccgaaaagggtgaagtagagaaataaagtctccccgctgaactact  657

ATGAGGTCAGAAGCCTTGCTGCTATATTTCACACTGCTACACTTTGCTGGGGCTGGTTTC  717
 M  R  S  E  A  L  L  L  Y  F  T  L  L  H  F  A  G  A  G  F
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 P  E  D  S  E  P  I  S  I  S  H  G  N  Y  T  K  Q  Y  P  V
TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG  837
 F  V  G  H  K  P  G  R  N  T  T  Q  R  H  R  L  D  I  Q  M
ATTATGATCATGAACGGAACCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT  897
 I  M  I  M  N  G  T  L  Y  I  A  A  R  D  H  I  Y  T  V  D
ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAAACTGACATGGAAATCTAGA  957
 I  D  T  S  H  T  E  E  I  Y  C  S  K  K  L  T  W  K  S  R
CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACTTT 1017
 Q  A  D  V  D  T  C  R  M  K  G  K  H  K  D  E  C  H  N  F
ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACTAATGCCTTC 1077
 I  K  V  L  L  K  K  N  D  D  A  L  F  V  C  G  T  N  A  F
AACCCTTCCTGCAGAAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGC 1137
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GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA 1197
 G  M  A  R  C  P  Y  D  A  K  H  A  N  V  A  L  F  A  D  G
AAACTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT 1237
 K  L  Y  S  A  T  V  T  D  F  L  A  I  D  A  V  I  Y  R  S
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 Y  F  V  Q  A  V  D  Y  G  D  Y  I  Y  F  F  F  R  E  I  A
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 V  E  Y  N  T  M  G  K  V  V  F  P  R  V  A  Q  V  C  K  N
GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTCCTGAAGGCGCGC 1477
 D  M  G  G  S  Q  R  V  L  E  K  Q  W  T  S  F  L  K  A  R
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 L  N  C  S  V  P  G  D  S  H  F  Y  F  N  I  L  Q  A  V  T
GATGTGATTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTTCTACACCTTATAAC 1597
 D  V  I  R  I  N  G  R  D  V  V  L  A  T  F  S  T  P  Y  N
AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACT 1657
 S  I  P  G  S  A  V  C  A  Y  D  M  L  D  I  A  S  V  F  T
```

Fig. 2 (cont.)

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GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA  1717
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GTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAACC  1777
 V  P  K  P  R  P  G  C  C  A  G  S  S  S  L  E  R  Y  A  T
TCCAATGAGTTCCCTGATGATACCCTGAACTTCATCAAGACGCACCCGCTCATGGATGAG  1837
 S  N  E  F  P  D  D  T  L  N  F  I  K  T  H  P  L  M  D  E
GCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTT  1897
 A  V  P  S  I  F  N  R  P  W  F  L  R  T  M  V  R  Y  R  L
ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG  1957
 T  K  I  A  V  D  T  A  A  G  P  Y  Q  N  H  T  V  V  F  L
GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTA  2017
 G  S  E  K  G  I  I  L  K  F  L  A  R  I  G  N  S  G  F  L
AATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTACAACTCTGAAAAATGCAGCTATGAT  2077
 N  D  S  L  F  L  E  E  M  S  V  Y  N  S  E  K  C  S  Y  D
GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT  2137
 G  V  E  D  K  R  I  M  G  M  Q  L  D  R  A  S  S  S  L  Y
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 V  A  F  S  T  C  V  I  K  V  P  L  G  R  C  E  R  H  G  K
TGTAAAAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGT  2257
 C  K  K  T  C  I  A  S  R  D  P  Y  C  G  W  I  K  E  G  G
GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC  2317
 A  C  S  H  L  S  P  N  S  R  L  T  F  E  Q  D  I  E  R  G
AATACAGATGGTCTGGGGGACTGTCACAATTCCTTTGTGGCACTGAATGGGCATTCCAGT  2377
 N  T  D  G  L  G  D  C  H  N  S  F  V  A  L  N  G  H  S  S
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GGAGGAATGCTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCACAGACCCTTTGGGG  2497
 G  G  M  L  D  W  K  H  L  L  D  S  P  D  S  T  D  P  L  G
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 V  A  V  V  Q  R  K  E  K  E  L  T  H  S  R  R  G  S  M  S
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 S  V  T  K  L  S  G  L  F  G  D  T  Q  S  K  D  P  K  P  E
GCCATCCTCACGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAG  2857
 A  I  L  T  P  L  M  H  N  G  K  L  A  T  P  G  N  T  A  K
ATGCTCATTAAAGCAGACCAGCACCACCTGGACCTGACGGCCCTCCCCACCCCAGAGTCA  2917
 M  L  I  K  A  D  Q  H  H  L  D  L  T  A  L  P  T  P  E  S
ACCCCAACGCTGCAGCAGAAGCGGAAGCCCAGCCGCGGCAGCCGCGAGTGGGAGAGGAAC  2977
 T  P  T  L  Q  Q  K  R  K  P  S  R  G  S  R  E  W  E  R  N
CAGAACCTCATCAATGCCTGCACAAAGGACATGCCCCCCATGGGCTCCCCTGTGATTCCC  3037
 Q  N  L  I  N  A  C  T  K  D  M  P  P  M  G  S  P  V  I  P
```

Fig. 2 (cont.)

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ACGGACCTGCCCCTGCGGGCCTCCCCCAGCCACATCCCCAGCGTGGTGGTCCTGCCCATC   3097
 T  D  L  P  L  R  A  S  P  S  H  I  P  S  V  V  V  L  P  I
ACGCAGCAGGGCTACCAGCATGAGTACGTGGACCAGCCCAAAATGAGCGAGGTGGCCCAG   3157
 T  Q  Q  G  Y  Q  H  E  Y  V  D  Q  P  K  M  S  E  V  A  Q
ATGGCGCTGGAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAACATCTCAGC   3217
 M  A  L  E  D  Q  A  A  T  L  E  Y  K  T  I  K  E  H  L  S
AGCAAGAGTCCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCCCAAA   3277
 S  K  S  P  N  H  G  V  N  L  V  E  N  L  D  S  L  P  P  K
GTTCCACAGCGGGAGGCCTCCCTGGGTCCCCCGGGAGCCTCCCTGTCTCAGACCGGTCTA   3337
 V  P  Q  R  E  A  S  L  G  P  P  G  A  S  L  S  Q  T  G  L
AGCAAGCGGCTGGAAATGCACCACTCCTCTTCCTACGGGGTTGACTATAAGAGGAGCTAC   3397
 S  K  R  L  E  M  H  H  S  S  S  Y  G  V  D  Y  K  R  S  Y
CCCACGAACTCGCTCACGAGAAGCCACCAGGCCACCACTCTCAAAAGAAACAACACTAAC   3457
 P  T  N  S  L  T  R  S  H  Q  A  T  T  L  K  R  N  N  T  N
TCCTCCAATTCCTCTCACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGACAACCCGCCG   3517
 S  S  N  S  S  H  L  S  R  N  Q  S  F  G  R  G  D  N  P  P
CCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGGCC   3577
 P  A  P  Q  R  V  D  S  I  Q  V  H  S  S  Q  P  S  G  Q  A
GTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCGGGGCTG   3637
 V  T  V  S  R  Q  P  S  L  N  A  Y  N  S  L  T  R  S  G  L
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 K  R  T  P  S  L  K  P  D  V  P  P  K  P  S  F  A  P  L  S
ACATCCATGAAGCCCAATGATGCGTGTACATAAtcccaggggggaggggggtcaggtgtcga   3757
 T  S  M  K  P  N  D  A  C  T  *

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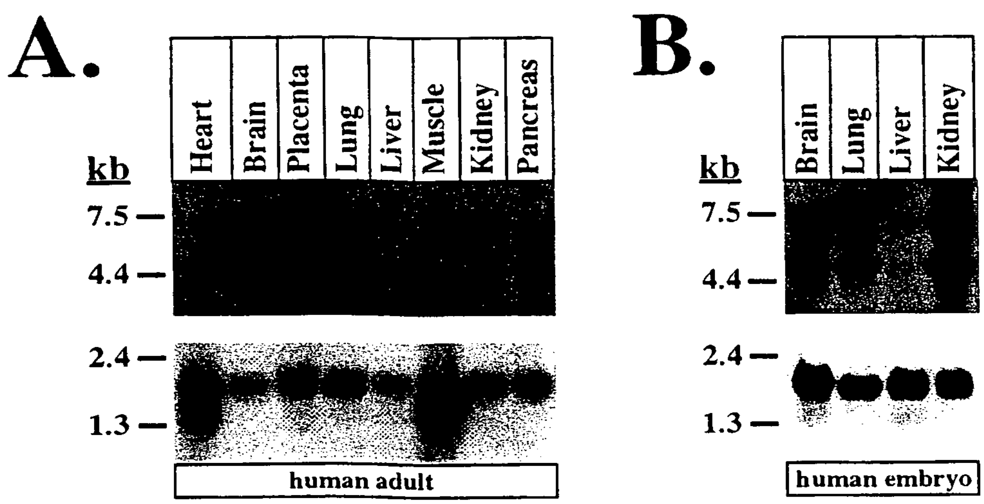
Fig. 3


A.
Heart
Brain
Placenta
Lung
Liver
Muscle
Kidney
Pancreas
kb
7.5
4.4
2.4
1.3
human adult
B.
Brain
Lung
Liver
Kidney
kb
7.5
4.4
2.4
1.3
human embryo

(MMU)Sema6A-1 Distribution in Mouse Adult and Embryonic Tissues

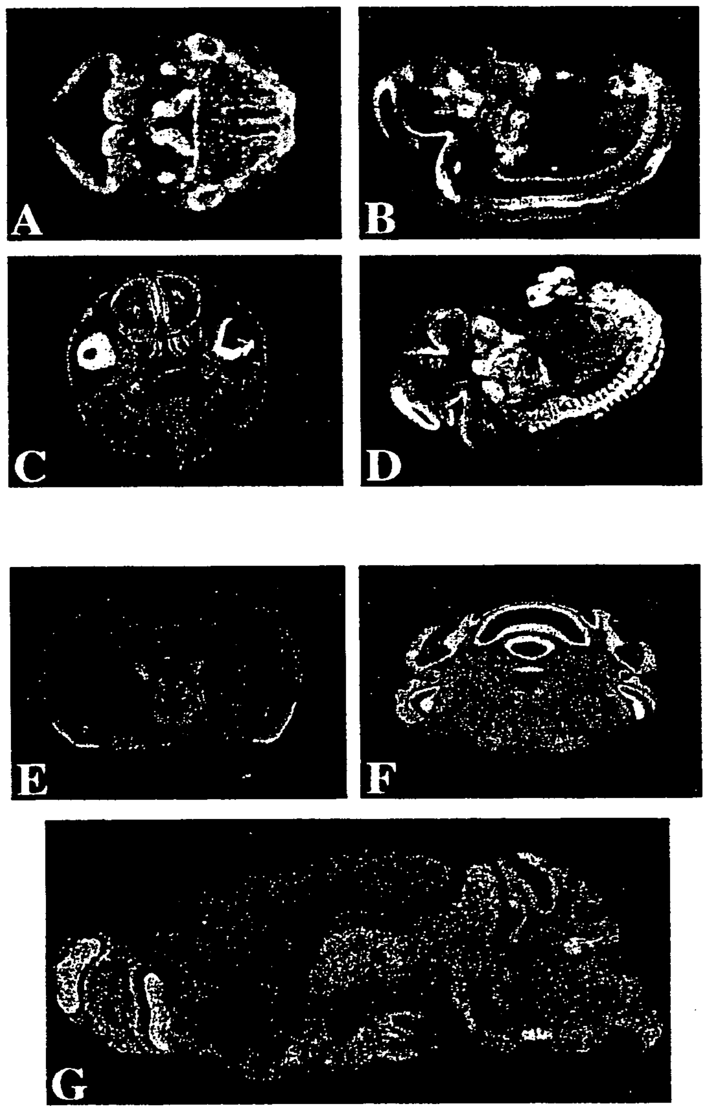


Fig. 4

(HSA)SEMA6A-1: Expression, Protein-Size and Dimerization

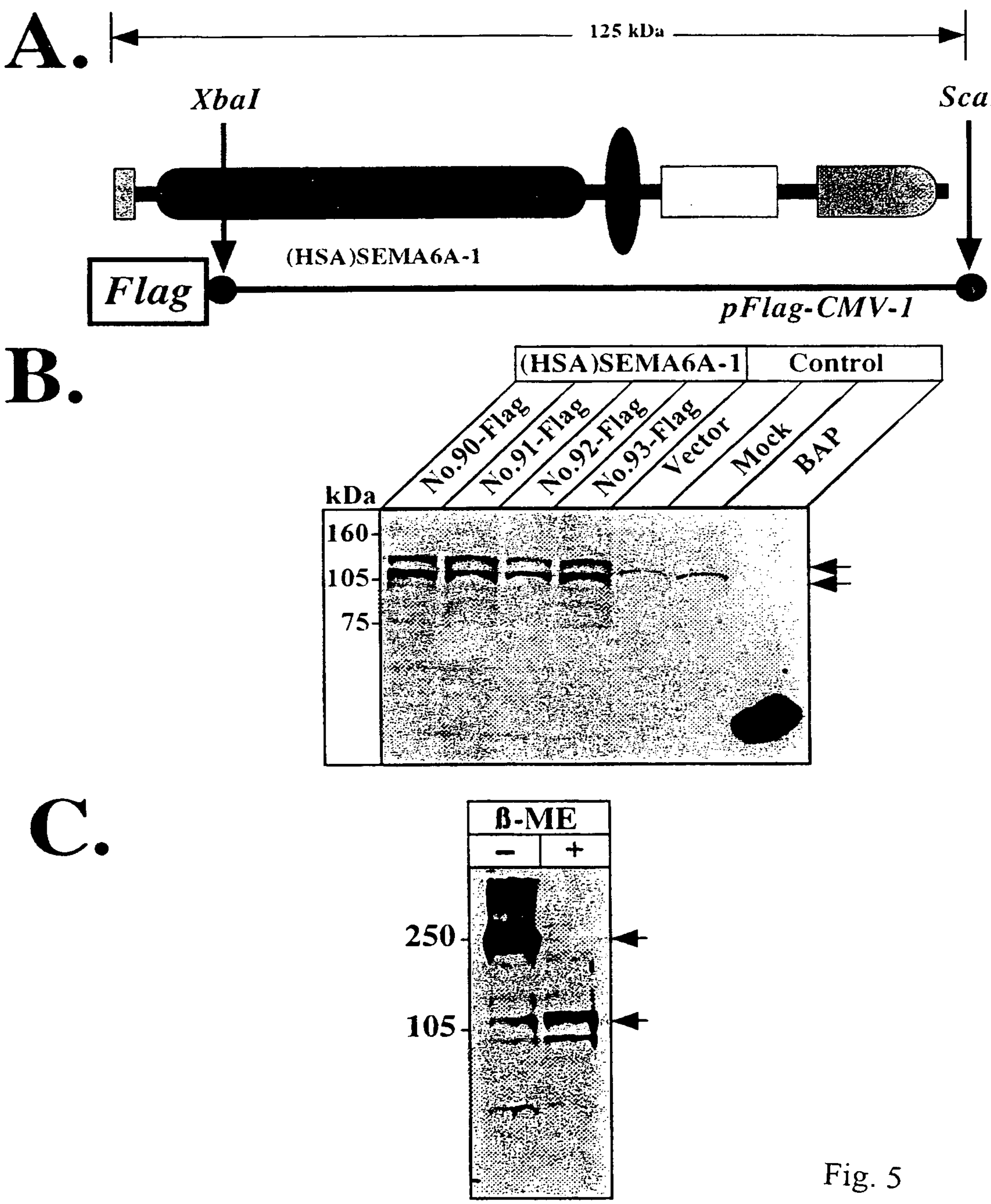


Fig. 5

Fig. 6

Sequence-Alignment: SEMA6A-1 / Zyxin

```
SEMA6A-1                                                                    (6a)
PPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPD-VPPKPSFAPLSTSMKPNDACT
* * ***    +* *  **  +    *  ** +++ *+  *   * + *+  *    *  * * *+ +    *
PPPQPQRKPQVQLH-VQPQAKP-HVQPQP-VSSANTQPRGPLSQAPTPAPKFAPVAPKFTPVVSKFSP
zyxin                                                                       (6b)
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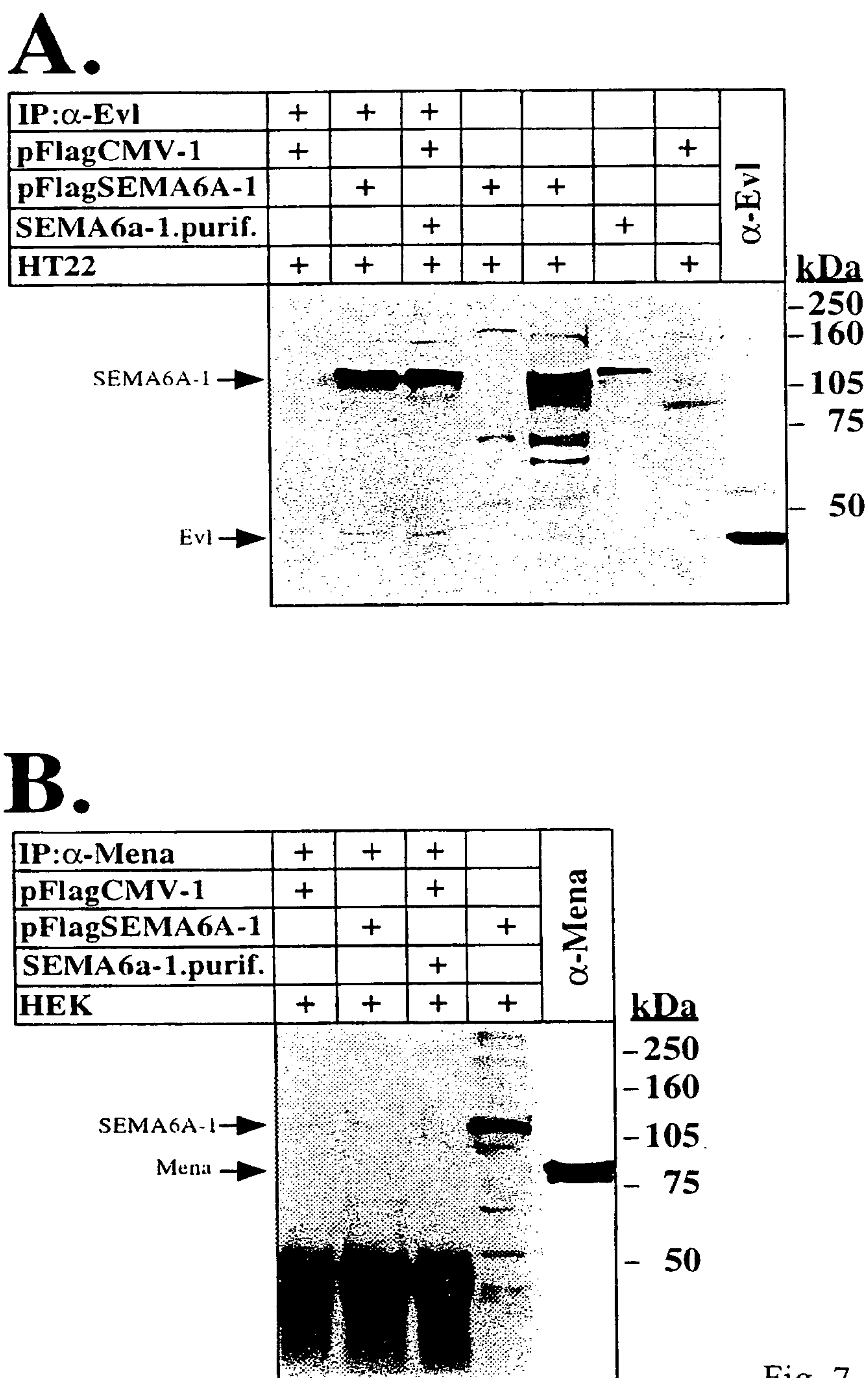
Identity: 33%
Similarity: 49%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pFlagSEMA6A-1
SEMA6a-1.purif.
HT22
α-Evl
kDa
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105
75
50
SEMA6A-1
Evl
B.
IP:α-Mena
pFlagCMV-1
pFlagSEMA6A-1
SEMA6a-1.purif.
HEK
α-Mena
kDa
250
160
105
75
50
SEMA6A-1
Mena

Fig. 7

Fig. 8

From Membrane to Cytoskeleton: Enabling a Connection

(Hu and Reichardt, Neuron, Vol. 22; March 1999)